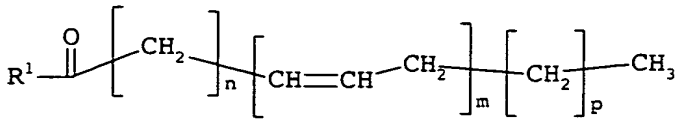
We claim:

1. A process for the production of compounds of the general formula I:



(I)

in transgenic plants with a content of at least 1% by weight based on the total fatty acids, which process comprises the following steps:

a) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with an Δ6-desaturase activity; and

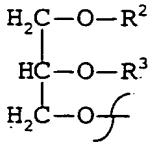
b) introducing at least one second nucleic acid sequence which encodes a polypeptide with a Δ 6-elongase activity; and,

c) if appropriate, introducing a third nucleic acid sequence which encodes a polypeptide with a Δ 5-desaturase activity;

d) followed by growing and harvesting the plants; and

where the variables and substituents in the formula I have the following meanings:

$R^1$ = -OH, coenzyme A (thioester), phosphatidylcholine, phosphatidylethanolamine, phoshatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycoshingolipid or a radical of the following general formula II

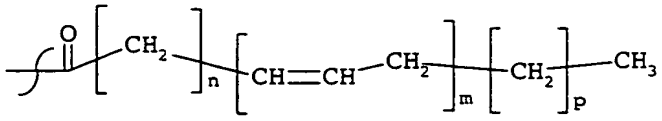


(II)

$R^2$ = H, phosphatidylcholine-, phosphatidylethanolamine-, phosphatidylglycerol-, diphosphatidylglycerol-, phosphatidylserine-, phosphatidylinositol-, shingolipid-, glycoshingolipid-, glycoshingolipid- or saturated or unsaturated $C_2$–$C_{24}$–alkylcarbonyl-,

$R^3$ = H, saturated or unsaturated $C_2$–$C_{24}$–alkylcarbonyl-, or

$R^2$ and $R^3$ independently of one another represent a radical of the general formula Ia



(Ia),

n = 3, 4 or 6, m = 3, 4 or 5 and p = 0 or 3.

2. The process according to claim 1, wherein the substituents $R^2$ and $R^3$ independently of one another are $C_{10}$-$C_{22}$-alkylcarbonyl-.

3. The process according to claim 1 or 2, wherein the substituents $R^2$ and $R^3$ independently of one another are $C_{16}$-, $C_{18}$-, $C_{20}$- or $C_{22}$-alkylcarbonyl-.

4. The method according to any of claims 1 to 3, wherein the substituents $R^2$ and $R^3$ independently of one another are unsaturated $C_{16}$-, $C_{18}$-, $C_{20}$- or $C_{22}$-alkylcarbonyl- with one, two, three, four or five double bonds.

5. The method according to any of claims 1 to 4, wherein the transgenic plant is an oil crop.

6. The method according to any of claims 1 to 5, wherein the transgenic plant is selected from the group consisting of soya, peanut, oilseed rape, canola, linseed, evening primrose, verbascum, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut or coconut.

7. The method according to any of claims 1 to 6, wherein the compounds of the formula I are obtained from the transgenic

plants in the form of their oils, fats, lipids or free fatty acids by pressing or extraction.

8. The process according to any of claims 1 to 7, wherein the oils, fats, lipids or free fatty acids obtained as claimed in claim 7 are refined.

9. The process according to any of claims 1 to 8, wherein the saturated or unsaturated fatty acids present in the compounds of the formula I are liberated.

10. The method according to any of claims 1 to 9, wherein the saturated or unsaturated fatty acids are liberated by alkaline hydrolysis or enzymatic cleavage.

11. The method according to any of claims 1 to 10, wherein the compounds of the general formula I are present in the transgenic plant at a content of at least 5% by weight, based on the total fatty acids.

12. The process according to any of claims 1 to 11, wherein the nucleic acid sequences which encode the polypeptides with Δ6-desaturase activity, Δ6-elongase activity or Δ5-desaturase activity are selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31,

b) nucleic acid sequences which, owing to the degeneracy of the genetic code, are obtained by back translation of the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32,

c) derivatives of the nucleic acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4,

SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32 and which have at least 50% homology at the amino acid level, without the enzymatic activity of the polypeptide being substantially reduced.

13. The process according to any of claims 1 to 12, wherein the nucleic acid sequences as claimed in claim 8 are linked with one or more regulatory signals in a nucleic acid construct.

14. The method according to any of claims 1 to 13, wherein the nucleic acid construct comprises additional biosynthetic genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allene oxide synthases, hydroperoxide lyases or fatty acid elongase(s).